

Appl. No. 10/520,497  
Amdt. dated September 12, 2005  
Preliminary Amendment

PATENT

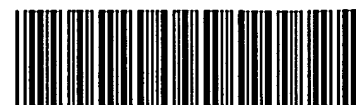
## **APPENDIX: Sequence Listing**

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,497  
Source: PLT  
Date Processed by STIC: 03/20/2006

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PCT

## RAW SEQUENCE LISTING

DATE: 03/20/2006

PATENT APPLICATION: US/10/520,497

TIME: 12:25:20

Input Set : A:\023070-127310US.ST25.txt

Output Set: N:\CRF4\03202006\J520497.raw

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3 <110> APPLICANT: The Regents of the University of California
4     Shi, Huazhong
5     Blumwald, Eduardo
7 <120> TITLE OF INVENTION: IMPROVED TRANSPORTERS AND THEIR USES
9 <130> FILE REFERENCE: 023070-127310US
11 <140> CURRENT APPLICATION NUMBER: US 10/520,497
C--> 12 <141> CURRENT FILING DATE: 2005-01-07
14 <150> PRIOR APPLICATION NUMBER: WO PCT/US2003/021549
15 <151> PRIOR FILING DATE: 2003-07-09
17 <150> PRIOR APPLICATION NUMBER: US 60/395,662
18 <151> PRIOR FILING DATE: 2002-07-12
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1614
26 <212> TYPE: DNA
27 <213> ORGANISM: Arabidopsis thaliana
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32 gttgcgttga atctctttgt tgcacttctt tgtgcttgta ttgttcttgg tcactctttg      120
34 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggg      180
36 gttaccattt tgttgattag taaaggaaaa agctcgcatc ttctcgctct tagtgaagat      240
38 cttttcttca tatatctttt gccacccatt atattcaatg caggggtttca agtaaaaaag      300
40 aagcagtttt tccgcaattt cgtgactatt atgctttttg gtgctgttgg gactattatt      360
42 tcttgacaaa tcatatctct aggtgtaaca cagttcttta agaagttgga cattggaacc      420
44 tttgacttgg gtgattatct tgctattggg gccatatatt ctgcaacaga ttcagtatgt      480
46 aactgcagg ttctgaatca agacgagaca cctttgcttt acagtcttgt attcggagag      540
48 ggtgttgtga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc      600
50 actcacctaa accacgaagc tgcttttcat cttcttgtaa acttcttgta tttgtttctc      660
52 ctaagtacct tgcttggtgc tgcaaccggt ctgataagtg cgtatgttat caagaagcta      720
54 tactttggaa ggcactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt      780
56 tcttatatgc ttgctgagct tttcgacttg agcggtatcc tcaactgtgtt tttctgtggt      840
58 attgtgatgt cccattacac atggcacaaat gtaacggaga gctcaagaat aacaacaaag      900
60 catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaatg      960
62 gatgccttgg acattgacaa gtggagatcc gtgagtgaac caccgggaac atcgatcgca      1020
64 gtgagctcaa tcctaattggg tctggtcatt gttggaagag cagcggtcgt ctttccgtta      1080
66 tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag      1140
68 gttgtgattt ggtggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac      1200
70 aagtttacaa gggccgggca cacagatgta cgcgggaatg caatcatgat cagcagtagc      1260
72 ataactgtct gtctttttag cacagtgggtg tttggatatg tgaccaaacc actcataagc      1320
74 tacctattac cgcaccagaa cgccaccacg agcatgttat ctgatgacaa cccccaaaaa      1380
76 tccatacata tccctttgtt ggaccaagac tcgttcattg agccttcagg gaaccacaat      1440
78 gtgcctcggc ctgacagtat acgtggcttc ttgacacggc ccactcgaac cgtgcattac      1500

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80 tactggagac aatttgatga ctccctcatg cgacccgtct ttggaggctcg tggctttgta 1560
82 ccctttgttc caggttctcc aactgagaga aaccctcctg atcttagtaa ggct 1614
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 538
87 <212> TYPE: PRT
88 <213> ORGANISM: Arabidopsis thaliana
90 <400> SEQUENCE: 2
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93 1 5 10 15
96 His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
97 20 25 30
100 Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
101 35 40 45
104 Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
105 50 55 60
108 Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
109 65 70 75 80
112 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
113 85 90 95
116 Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
117 100 105 110
120 Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
121 115 120 125
124 Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
125 130 135 140
128 Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
129 145 150 155 160
132 Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
133 165 170 175
136 Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
137 180 185 190
140 Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
141 195 200 205
144 Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
145 210 215 220
148 Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
149 225 230 235 240
152 Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
153 245 250 255
156 Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
157 260 265 270
160 Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
161 275 280 285
164 His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
165 290 295 300
168 Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
169 305 310 315 320
172 Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
173 325 330 335

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176 Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
177          340          345          350
180 Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
181          355          360          365
184 Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
185          370          375          380
188 Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
189 385          390          395          400
192 Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
193          405          410          415
196 Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
197          420          425          430
200 Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
201          435          440          445
204 Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
205          450          455          460
208 Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
209 465          470          475          480
212 Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
213          485          490          495
216 Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
217          500          505          510
220 Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
221          515          520          525
224 Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
225          530          535

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228 &lt;210&gt; SEQ ID NO: 3

229 &lt;211&gt; LENGTH: 1614

230 &lt;212&gt; TYPE: DNA

231 &lt;213&gt; ORGANISM: Artificial

233 &lt;220&gt; FEATURE:

234 &lt;223&gt; OTHER INFORMATION: Modified AtNHX1 SM-23

236 &lt;400&gt; SEQUENCE: 3

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237 atgttggtgatt ctctagtgtc gaaactgcct tcgttatcga catctgatca cgcttctgtg      60
239 gttgcgttga atctctttgt tgcacttctt tgtgcttgta ttgttcttgg tcatcttttg      120
241 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggg      180
243 gttaccatgtt tgttgattag taaaggaaaa agctcgcac tctcgtctt tagtgaagat      240
245 cttttcttca tatactcttt gccacccatt atattcaatg cagggtttca agtaaaaaag      300
247 aagcagtttt tccgcaattt cgtgactatt atgctttttg gtgctgttgg gactattatt      360
249 tcttgacaaa tcatatctct aggtgtaaca cagttcttta agaagtggga cattggaacc      420
251 tttgacttgg gtgattatct tgctattggg gccatatttg ctgcaacaga ttcagtatgt      480
253 aactgacagg ttctgaatca agacgagaca cctttgcttt acagtcttgt attcggagag      540
255 ggtgttgatga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc      600
257 actcacctaa accacgaagc tgcttttcat cttcttggaa acttcttgta tttgtttctc      660
259 ctaagtacat tgcttgggtg tgcaaccggg ctgataagtg cgtatgttat caagaagcta      720
261 tactttggaa ggcactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt      780
263 tcttatatgc ttgctgagct ttctgacttg agcggtatcc tctactgtgt tttctgtggg      840
265 attgtgatgt cccattacac atggcacaa gtaacggaga gctcaagaat aacaacaaa      900
267 catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaatg      960

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## RAW SEQUENCE LISTING

DATE: 03/20/2006

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269 gatgccttgg acattgacaa gtggagatcc gtgagtgaca caccgggaac atcgatcgca 1020
271 gtgagctcaa tcctaattggg tctgggtcatg gttggaagag cagcgttcgt ctttccgtta 1080
273 tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag 1140
275 gttgtgattt ggtgggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac 1200
277 aagttttacaa gggccgggca cacagatgta cgcgggaatg caatcatgat caccgagtacg 1260
279 ataactgtct gtcttttttag cacagtgggtg tttgggtatgc tgaccaaacc actcataagc 1320
281 tacctattac cgcaccagaa cgccaccacg agcatgttat ctgatgacaa caccctcaaaa 1380
283 tccatacata tccctttgtt ggaccaagac tcgttcattg agccttcagg gaaccacaat 1440
285 gtgcctcggc ctgacagtat acgtggcttc ttgacacggc ccactcgaac cgtgcattac 1500
287 tactggagac aatttgatga ctgcttcattg cgaccctgtc ttggaggtcg tggctttgta 1560
289 ccctttgttc caggttctcc aactgagaga aaccctcctg atcttagtaa ggct 1614

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292 &lt;210&gt; SEQ ID NO: 4

293 &lt;211&gt; LENGTH: 538

294 &lt;212&gt; TYPE: PRT

295 &lt;213&gt; ORGANISM: Artificial

297 &lt;220&gt; FEATURE:

298 &lt;223&gt; OTHER INFORMATION: Putative amino acid sequence encoded by modified AtNHX1 SM-

23

300 &lt;400&gt; SEQUENCE: 4

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303 1 5 10 15
306 His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
307 20 25 30
310 Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
311 35 40 45
314 Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
315 50 55 60
318 Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
319 65 70 75 80
322 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
323 85 90 95
326 Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
327 100 105 110
330 Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
331 115 120 125
334 Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
335 130 135 140
338 Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
339 145 150 155 160
342 Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
343 165 170 175
346 Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
347 180 185 190
350 Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
351 195 200 205
354 Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
355 210 215 220
358 Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
359 225 230 235 240
362 Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu

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## RAW SEQUENCE LISTING

DATE: 03/20/2006

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Input Set : A:\023070-127310US.ST25.txt

Output Set: N:\CRF4\03202006\J520497.raw

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363          245          250          255
366 Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
367          260          265          270
370 Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
371          275          280          285
374 His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
375          290          295          300
378 Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
379 305          310          315          320
382 Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
383          325          330          335
386 Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
387          340          345          350
390 Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
391          355          360          365
394 Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
395          370          375          380
398 Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
399 385          390          395          400
402 Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
403          405          410          415
406 Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
407          420          425          430
410 Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
411          435          440          445
414 Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
415          450          455          460
418 Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
419 465          470          475          480
422 Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
423          485          490          495
426 Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Cys Phe Met Arg Pro
427          500          505          510
430 Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
431          515          520          525
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435          530          535
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441 <213> ORGANISM: Artificial
443 <220> FEATURE:
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451 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcaactggt      180
453 gttaccattt tggtgattag taaaggaaaa agctcgcacg ttctcgtctt tagtgaagat      240
455 cttttcttca tatatctttt gccacccatt atattcaatg cagggtttca agtaaaaaag      300

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